



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: DeBonte, L. et al.
- (ii) TITLE OF INVENTION: PLANTS HAVING MUTANT SEQUENCES THAT CONFER ALTERED FATTY ACID PROFILES
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson, P.C., P.A.
 - (B) STREET: 60 South Sixth Street, Suite 3300
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/416,497
 - (B) FILING DATE: 04-APR-1995
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/170,886
 - (B) FILING DATE: 21-DEC-1993
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/739,965
 - (B) FILING DATE: 05-AUG-1991
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/575,542
 - (B) FILING DATE: 30-AUG-1990
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ellinger, Mark S.
 - (B) REGISTRATION NUMBER: 34,812
 - (C) REFERENCE/DOCKET NUMBER: A21-535.10
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612/335-5070
 - (B) TELEFAX: 612/288-9696
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA

| (iii) | HYPOTHETICAL: NO |
|-------|------------------|
| (iv) | ANTI-SENSE: NO |
| (vi) | ORIGINAL SOURCE: |
| | (A) ORGANISM: E |

ORIGINAL SOURCE:
(A) ORGANISM: Brassica napus

(ix) FEATURE:

(D) OTHER INFORMATION: Wild type D form.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 |
|--|
| Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 20 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 40 ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 60 TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CTC CTC CTC CTC CAC CCT Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 80 CTC TCC TAC TTC GCC TGG CCT CTC TAC TGC GGC CAA GGG TGC GTC Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 CTA ACC GGC GTC TGG GTC ATA GCC CAC GAA TGC GGC CAC CAC GAC TTC Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 100 AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CTC ATC TCC CTC CTC CTC CTC CTC CTC CT |
| Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 55 |
| THE Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 55 TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CTC CTC CTC CTC CAC CCT CAC CCT CS Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 65 CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC CTA ACC Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 95 CTA ACC GGC GTC TGG GTC ATA GCC CAC GAA TGC GGC CAC GAC GCC TTC ACC TGT ACC TGT ACC GGC GTC CTA ACC GGC GTC TGG ATA GCC CAC GAA TGC GGC CAC CAC GCC TTC ACC TGT ACC TGT ACC TGG GTC CTC TAC TTC ACC TGC GTC CTC TAC TTC ACC TGC ASP Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 120 TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC ACT CTC ACC TCC ACC ACC GCC CAC ACC ACC GCC TGC ASP Tyr Gln Trp Leu Asp Asp Trp Lys Tyr Ser His Arg Ser His 130 CAT TCC AAC ACT GGC TCC CTC GAC ACA GAC ACC GCC ACC ACC CAC ACC AC |
| Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 80 CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 95 CTA ACC GGC GTC TGG GTC ATA GCC CAC GAA TGC GGC CAC CAC GCC TTC Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 110 AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 125 TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC CAC GAC CAC GAC TCC TTC Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His 130 CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAC GAC GAC GAC GAC GAC GA |
| Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Strong Growth Strong Grows At Act Growth Strong G |
| Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 100 AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 120 TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His 130 CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 145 AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC GTT CGT G24 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg |
| Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 120 TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His 130 CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 160 AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC ACC CCT TTG Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 170 GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC GCC TTC CGT TYr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg |
| Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His 130 CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 160 AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 175 GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 190 TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT ATG Lys Lys Arg Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg |
| His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 160 AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 175 GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg |
| Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 175 GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg |
| Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190 TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT 77r Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg |
| Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg |
| |

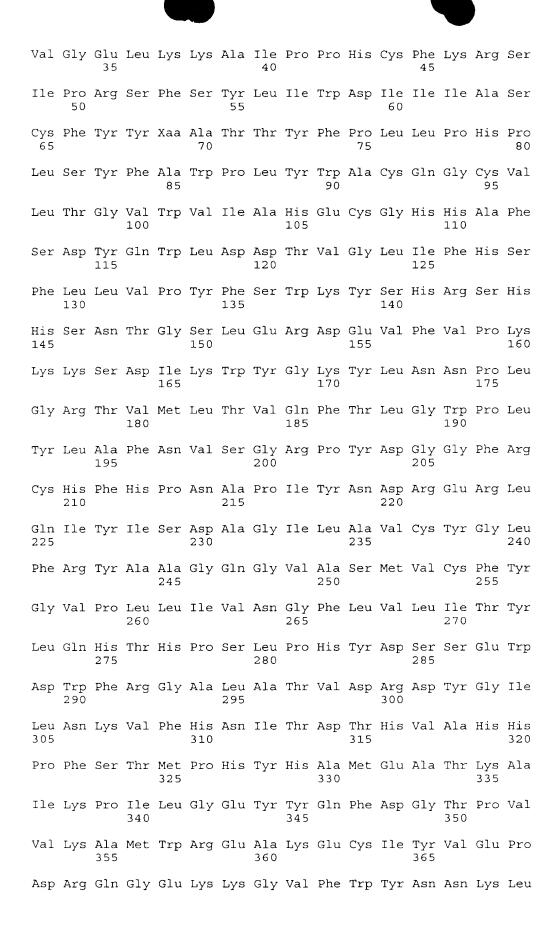
| | | | | | | | CGT Arg | | 672 |
|----|--|--|--|--|--|--|-------------------|---|------|
| | | | | | | | GGT Gly | | 720 |
| | | | | | | | TTC Phe 255 | | 768 |
| | | | | | | | ACT Thr | | 816 |
| | | | | | | | GAG Glu | | 864 |
| | | | | | | | GGA Gly | | 912 |
| | | | | | | | CAT His | | 960 |
| | | | | | | | AAG Lys 335 | | 1008 |
| | | | | | | | CCG Pro | | 1056 |
| | | | | | | | GAA Glu | | 1104 |
| | | | | | | | AAG Lys | Т | 1153 |
| GA | | | | | | | | | 1155 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 5 10 15

Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr



370 375 380

| (2) | INFORMATION | FOR | SEO | ID | NO:3: |
|-----|-------------|-----|-----|----|-------|

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Brassica napus
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: IMC129
- (ix) FEATURE:
- (D) OTHER INFORMATION: ${\tt G}$ to A transversion mutation at nucleotide 316 of the D form.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| ,,,,, | , | | | | ~ | | | | | |
|-------|---|-----|------|------------------|-------|---|-----|--|--|-----|
| | | | | ATG Met | | | | | | 48 |
| | | | | CGC Arg | | | | | | 96 |
| | | | | GCA Ala | | | | | | 144 |
| | | | | TAC Tyr 55 | | | | | | 192 |
| | | | | ACC Thr | _ | - | | | | 240 |
| | | | | CCT Pro | | | | | | 288 |
| | | | | ATA Ile | | | | | | 336 |
| | | Gln | Leu | GAC Asp | Thr | | Gly | | | 384 |

432

TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His

135

| | | | TCC Ser 150 | | | | | | | 480 |
|----|--|--|-------------------|--|--|--|--|------------|---|------|
| | | | AAG Lys | | | | | | | 528 |
| | | | TTA Leu | | | | | | | 576 |
| | | | GTC Val | | | | | | | 624 |
| | | | AAC Asn | | | | | | | 672 |
| | | | GAC Asp 230 | | | | | | | 720 |
| | | | GGC Gly | | | | | | | 768 |
| | | | ATT Ile | | | | | | | 816 |
| | | | CCT Pro | | | | | | | 864 |
| | | | GCT Ala | | | | | | | 912 |
| | | | CAC His 310 | | | | | | | 960 |
| | | | CCG Pro | | | | | _ | | 1008 |
| | | | GGA Gly | | | | | | | 1056 |
| | | | AGG Arg | | | | | | | 1104 |
| | | | AAG Lys | | | | | TTA Leu | Т | 1153 |
| GA | | | | | | | | | | 1155 |

⁽²⁾ INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His 135 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 170 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 185 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 235 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 280 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile

| | 290 | | | | | 295 | | | | | 300 | | | | | |
|--------------------------------------|--|---------------------------------------|--|---|---|--|--|---|--|--|--|------------------------------------|--------------------------------|---------------------------------------|-----------------------------|-----------|
| Leu 305 | Asn | Lys | Val | Phe | His 310 | Asn | Ile | Thr | Asp | Thr 315 | His | Val | Ala | His | His 320 | |
| Pro | Phe | Ser | Thr | Met 325 | Pro | His | Tyr | His | Ala 330 | Met | Glu | Ala | Thr | Lys 335 | Ala | |
| Ile | Lys | Pro | Ile 340 | Leu | Gly | Glu | Tyr | Tyr 345 | Gln | Phe | Asp | Gly | Thr 350 | Pro | Val | |
| Val | Lys | Ala 355 | Met | Trp | Arg | Glu | Ala 360 | Lys | Glu | Cys | Ile | Tyr 365 | Val | Glu | Pro | |
| Asp | Arg 370 | Gln | Gly | Glu | Lys | Lys 375 | Gly | Val | Phe | Trp | Tyr 380 | Asn | Asn | Lys | Leu | |
| (2) | |) SE((1 (1 | QUENCA) LI B) TI C) SI | CE CI ENGTI YPE: IRANI | HARACH: 11 nucl | ID N CTERI 155 h Leic ESS: line | STIC pase acic sing | CS: pain | rs | | | | | | | |
| | (ii) |) MOI | LECUI | LE T | YPE: | DNA | | | | | | | | | | |
| | (iii) | HYI | РОТНІ | ETICA | 1 : LA | 10 | | | | | | | | | | |
| | (iv) |) AN | rı-sı | ENSE | : NO | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | |
| | (vi) | | | | OURCE ISM: | E: Bras | ssica | a nap | pus | | | | | | | |
| | | (<i>)</i> FE | A) OI ATURI | RGANI E: | ISM: | | | | | ype I | F foi | cm. | | | | |
| | (ix) | () FE) (I | A) OI ATURI O) O' | RGANI E: THER | ISM: | Bras | rion | : Wil | ld ty | | F for | cm. | | | | |
| | (ix) | () FEA (I SEQ GCA | A) OI ATURI O) OI QUENG GGT | RGANI E: THER CE DI GGA | ISM: INFO ESCRI AGA | Bras | TION ON: S CAA | : Wil | ld ty ID NO TCT | D:5: CCT | CCC | TCC | | | | 48 |
| Met 1 GAA | (ix) (xi) GGT Gly ACC | (i) FEA (I) SEG GCA Ala | A) ON ATURN O) OT QUENC GGT Gly AAC | RGAN: E: THER CE DE GGA Gly 5 | ISM: INFO ESCRI AGA Arg | Bras ORMAT IPTIC ATG | CAA Gln | E William SEQ TG GTG Val | ld ty ID NO TCT Ser 10 TGC | CCT Pro | CCC Pro | TCC Ser | Lys | Lys 15 TTC | Ser | 48 96 |
| Met 1 GAA Glu GTC | (ix) (xi) GGT Gly ACC Thr | GAC ASP | A) OI ATURI D) O' QUENC GGT Gly AAC Asn 20 | RGANI E: FHER CE DI GGA Gly 5 ATC Ile AAG | ISM: INFO ESCRI AGA Arg AAG Lys | Bras ORMAT IPTIC ATG Met CGC | CAA Gln GTA Val | GTG Val | ld ty ID NO TCT Ser 10 TGC Cys | CCT Pro GAG Glu | CCC Pro ACA Thr | TCC Ser CCG Pro | CCC Pro 30 | Lys 15 TTC Phe | Ser ACT Thr | |
| Met 1 GAA Glu GTC Val | (ix) (xi) GGT Gly ACC Thr GGA Gly CCT | GCA Ala GAC Asp GAA Glu 35 CGC | ATURED) OF QUENC GGT Gly AAC Asn 20 CTC Leu | RGAN: E: THER CE DH GGA Gly 5 ATC Ile AAG Lys | ISM: INFO ESCRI AGA Arg AAG Lys AAA Lys | Bras ORMAT IPTIC ATG Met CGC Arg | CAA Gln GTA Val ATC Ile 40 CTC | : Will SEQ : GTG Val CCC Pro 25 CCA Pro | Id ty ID NO TCT Ser 10 TGC Cys CCG Pro | CCT Pro GAG Glu CAC His | CCC Pro ACA Thr TGT Cys | TCC Ser CCG Pro TTC Phe 45 | CCC Pro 30 AAA Lys | Lys 15 TTC Phe CGC Arg | Ser ACT Thr TCG Ser TCC | 96 |
| Met 1 GAA Glu GTC Val ATC Ile | (ix) (xi) GGT Gly ACC Thr GGA Gly CCT Pro 50 TTC | GCA Ala GAC Asp GAA Glu 35 CGC Arg | A) ON ATURN D) OT QUENC GGT Gly AAC ASN 20 CTC Leu TCT Ser | RGAN: E: THER CE DH GGA Gly 5 ATC Ile AAG Lys TTC Phe | ISM: INFO ESCRI AGA Arg AAG Lys AAA Lys TCC Ser | DRMATO ATG Met CGC Arg GCA Ala | CAA Gln GTA Val ATC Ile 40 CTC Leu ACT | GTG Val CCC Pro 25 CCA Pro ATC Ile | Id ty ID NO TCT Ser 10 TGC Cys CCG Pro TGG Trp | CCT Pro GAG Glu CAC His GAC Asp | CCC Pro ACA Thr TGT Cys ATC 11e 60 CTC | TCC Ser CCG Pro TTC Phe 45 ATC Ile | CCC Pro 30 AAA Lys ATA Ile CCT | Lys 15 TTC Phe CGC Arg | ACT Thr TCG Ser TCC Ser CCT | 96 144 |

| | | | | CAC His 105 | | | | 336 |
|--|--|--|--|-------------------|--|--|--|------|
| | | | | ACC Thr | | | | 384 |
| | | | | TGG Trp | | | | 432 |
| | | | | AGA Arg | | | | 480 |
| | | | | GGC Gly | | | | 528 |
| | | | | CAG Gln 185 | | | | 576 |
| | | | | AGA Arg | | | | 624 |
| | | | | ATC Ile | | | | 672 |
| | | | | ATC Ile | | | | 720 |
| | | | | GTT Val | | | | 768 |
| | | | | GGG Gly 265 | | | | 816 |
| | | | | CCT Pro | | | | 864 |
| | | | | ACC Thr | | | | 912 |
| | | | | ACG Thr | | | | 960 |
| | | | | CAT His | | | | 1008 |
| | | | | TAT Tyr 345 | | | | 1056 |

| | | | | | | | GAA Glu | | 1104 |
|----|------|-------|------|------|------|------|----------------|-------|------|
| | Gln | - | | | | | AAG Lys | T | 1153 |
| GA | | | | | | | | | 1155 |

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

| | () | (i) S | SEQUE | ENCE | DESC | CRIPT | CION: | SEÇ | O ID | NO:6 | 5: | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met 1 | Gly | Ala | Gly | Gly 5 | Arg | Met | Gln | Val | Ser 10 | Pro | Pro | Ser | Lys | Lys 15 | Ser |
| Glu | Thr | Asp | Asn 20 | Ile | Lys | Arg | Val | Pro 25 | Cys | Glu | Thr | Pro | Pro 30 | Phe | Thr |
| Val | Gly | Glu 35 | Leu | Lys | Lys | Ala | Ile 40 | Pro | Pro | His | Cys | Phe 45 | Lys | Arg | Ser |
| Ile | Pro 50 | Arg | Ser | Phe | Ser | Tyr 55 | Leu | Ile | Trp | Asp | Ile 60 | Ile | Ile | Ala | Ser |
| Cys 65 | Phe | Tyr | Tyr | Val | Ala 70 | Thr | Thr | Tyr | Phe | Pro 75 | Leu | Leu | Pro | His | Pro 80 |
| Leu | Ser | Tyr | Phe | Ala 85 | Trp | Pro | Leu | Tyr | Trp 90 | Ala | Cys | Gln | Gly | Cys 95 | Val |
| Leu | Thr | Gly | Val 100 | Trp | Val | Ile | Ala | His 105 | Glu | Cys | Gly | His | His 110 | Ala | Phe |
| Ser | Asp | Tyr 115 | Gln | Trp | Leu | Asp | Asp 120 | Thr | Val | Gly | Leu | Ile 125 | Phe | His | Ser |
| Phe | Leu 130 | Leu | Val | Pro | Tyr | Phe 135 | Ser | Trp | Lys | Tyr | Ser 140 | His | Arg | Arg | His |
| His 145 | Ser | Asn | Thr | Gly | Ser 150 | Leu | Glu | Arg | Asp | Glu 155 | Val | Phe | Val | Pro | Lys 160 |
| Lys | Lys | Ser | Asp | Ile 165 | Lys | Trp | Tyr | Gly | Lys 170 | Tyr | Leu | Asn | Asn | Pro 175 | Leu |
| Gly | Arg | Thr | Val 180 | Met | Leu | Thr | Val | Gln 185 | Phe | Thr | Leu | Gly | Trp 190 | Pro | Leu |

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu

200

215

195

210

205

 Gln
 Ile
 Tyr
 Ile
 Ser
 Asp 230
 Ala
 Gly
 Ile
 Leu 235
 Val
 Cys
 Tyr
 Gly
 Leu 240

 Tyr
 Arg
 Tyr
 Ala
 Ala Ala 245
 Val
 Gly
 Val
 Ala Ser
 Met
 Val
 Cys
 Phe
 Tyr

 Gly
 Val
 Pro
 Leu Leu 11e
 Val
 Asn
 Gly Phe
 Leu Val
 Leu Ile
 Tyr
 Tyr

 Leu
 Gln
 His
 Thr
 His
 Pro
 Ser Leu Phe
 Pro
 His
 Tyr
 Asp Ser Ser Ser Glu
 Trp

 Leu
 Asn
 Lys
 Arg
 Gly
 Ala
 Leu Pro
 His
 Tyr
 Asp Arg
 Asp Tyr
 Gly
 Ile
 Tyr

 Leu
 Asn
 Lys
 Asn
 Ile
 Thr
 Asp Tyr
 Asp Tyr
 Ala
 His
 Tyr
 Asp Tyr
 Asp Tyr
 Ala
 His
 Tyr
 Asp Tyr
 Asp Tyr
 Asp Tyr
 Asp Tyr
 Asp Tyr</t

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Brassica napus
- (ix) FEATURE:
- (D) OTHER INFORMATION: T to A transversion mutation at nucleotide 515 of the F form.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser

1 5 10 15

GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr

20 25 30

| | | | | | | | ATC Ile 40 | | | | | | | | | 144 |
|------------|-------------------|-------------------|-------------------|------------|------------|-------------------|-------------------|-------------------|------------|------------|-------------------|-------------------|-------------------|------------|------------|-----|
| | | | | | | | CTC Leu | | | | | | | | | 192 |
| | | | | | | | ACT Thr | | | | | | | | | 240 |
| | | | | | | | CTC Leu | | | | | | | | | 288 |
| | | | | | | | GCC Ala | | | | | | | | | 336 |
| AGC Ser | GAC Asp | TAC Tyr 115 | CAG Gln | TGG Trp | CTG Leu | GAC Asp | GAC Asp 120 | ACC Thr | GTC Val | GGC Gly | CTC Leu | ATC Ile 125 | TTC Phe | CAC His | TCC Ser | 384 |
| | | | | | | | TCC Ser | | | | | | | | | 432 |
| | | | | | | | GAG Glu | | | | | | | | | 480 |
| | | | | | | | TAC Tyr | | | | | | | | | 528 |
| GGA Gly | CGC Arg | ACC Thr | GTG Val 180 | ATG Met | TTA Leu | ACG Thr | GTT Val | CAG Gln 185 | TTC Phe | ACT Thr | CTC Leu | GGC Gly | TGG Trp 190 | CCT Pro | TTG Leu | 576 |
| TAC Tyr | TTA Leu | GCC Ala 195 | TTC Phe | AAC Asn | GTC Val | TCG Ser | GGG Gly 200 | AGA Arg | CCT Pro | TAC Tyr | GAC Asp | GGC Gly 205 | GGC Gly | TTC Phe | GCT Ala | 624 |
| TGC Cys | CAT His 210 | TTC Phe | CAC His | CCC Pro | AAC Asn | GCT Ala 215 | CCC Pro | ATC Ile | TAC Tyr | AAC Asn | GAC Asp 220 | CGC Arg | GAG Glu | CGT Arg | CTC Leu | 672 |
| | | | | | | | GGC Gly | | | | | | | | | 720 |
| | | | | | | | GGA Gly | | | | | | | | | 768 |
| | | | | | | | AAT Asn | | | | | | | | | 816 |
| | | | | | | | CTG Leu 280 | | | | | | | | | 864 |

| | | | | | | | GGA Gly | | | 912 |
|----|------|------|------|------|------|--|-------------------|------------|---|------|
| | | | | | | | CAT His | | | 960 |
| | | | | | | | AAG Lys 335 | | | 1008 |
| | | | | | | | CCG Pro | | | 1056 |
| | | | | | | | GAA Glu | | | 1104 |
| | | | | | | | AAG Lys | TTA Leu | Т | 1153 |
| GA | | | | | | | | | | 1155 |

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 5 10 15

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 50 55 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Pro His Pro 65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 130 $$135\$

